

PF 53896

SEQUENCE LISTING

<110> SunGene GmbH & Co.KGaA

<120> Transgenic expression cassettes for expressing nucleic acids
in nonreproductive floral tissues of plants

<130> PF53896-AT

<140>

<141>

<160> 36

<170> PatentIn Ver. 2.1

<210> 1

<211> 2039

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> promoter

<222> (1)..(2039)

<223> 76L promoter (including 5'-untranslated region) of
gene locus At3g01980

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<210> 2
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 <213> Arabidopsis thaliana
 <220>
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 <222> (1)..(2180)
 <223> 84L promoter (including 5'-untranslated region) of
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 agatactaca tgattaggcc gatggaacca aagatgagcg actcttcttg taacattgtg 360
 tttgctacgc aatgctcggg tttttttttt ttagatcgag actttgcctg agattctggg 420
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 <223> 76S promoter (including 5'-untranslated region) of
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<400> 3

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gttttcacaaa atccactacc ctcccaccac ctagaatctt ttgttaccta ccaacaccct 300
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aattaggaat cttggagatg gatccattag tagtaggata ataggatatg atggaatttg 660
gttggggaac agtgataact tacgcttgct tccggcgccg ggaaagtgtg aaaacctaca 720
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<211> 1097

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<213> *Arabidopsis thaliana*

<220>

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<223> 84S promoter (including 5'-untranslated region) of gene locus Atlg63140

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atcgatgtaa cacttttagga ttgaatcaat atgaaaagtt atacaccgaa tttgtgagaa 300
acgagtatag cttagacaaa atttgttttt cttaaattaa gcggaaaaat aattaaacag 360
agaccaaaatt aagcgttctt cttgaactga aatcactaaa gttaaagttaa cccgttagta 420
gagtgttaac tatttaaaca aagaaaactc caaacccaat tgagaaacta ctcaaacata 480
gaaacaacac ataatgattc agtagctacc aatatcata tcaactttgt ttcgattcct 540
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atcgcttatt accttaaaag cgtcctcaaa ccaacaaaaa caaaaatagt tgcatcaatg 720
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aacaatttta gaccattcac actgaatgag tatgactaac attcacattc acattcaatt 840
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aaatacgtgc ccataattta attaatattat atatttagct atcaaattat aggcaaatg 1020
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<222> (132)..(764)
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gene locus At3g01980

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acttttgcaa a atg gaa aat ccg gcg aag aga gtg ttg atg aca tcc aac 170
Met Glu Asn Pro Ala Lys Arg Val Leu Met Thr Ser Asn
1 5 10

ggc gac gag gtg tcc cga aac atc gct ttc cat cta gcc aaa cac ggt 218
Gly Asp Glu Val Ser Arg Asn Ile Ala Phe His Leu Ala Lys His Gly
15 20 25

tgc aag ttg gta atg atg gga aat gag ggt tcc cta agg agc att gta 266
Cys Lys Leu Val Met Met Gly Asn Glu Gly Ser Leu Arg Ser Ile Val
30 35 40 45

gac aag att aga gat tcc att gag gga gcc ttc cct gcc gat gtt ata 314
Asp Lys Ile Arg Asp Ser Ile Glu Gly Ala Phe Pro Ala Asp Val Ile
50 55 60

gca ctc gac atg gaa tct gac tct gaa gtt gct ttt cat gcc gct gtc 362
Ala Leu Asp Met Glu Ser Asp Ser Glu Val Ala Phe His Ala Ala Val
65 70 75

caa aag gca tgg gaa ctt tcc ggc cat ttc gat gct ttt ctc aac tct 410
Gln Lys Ala Trp Glu Leu Ser Gly His Phe Asp Ala Phe Leu Asn Ser
80 85 90

tat acc tac caa ggt tta att tgc ttc ttg ttt ttc act acc ctg cct 458
Tyr Thr Tyr Gln Gly Leu Ile Cys Phe Leu Phe Phe Thr Thr Leu Pro
95 100 105

ttg atg ctc ttg tgt gtt gat cat tcc ttt att caa caa tct ttc ttt 506
Leu Met Leu Leu Cys Val Asp His Ser Phe Ile Gln Gln Ser Phe Phe
110 115 120 125

ctt gca gga aag gtg cag gac att ctt caa gtc tct caa gat gag ttc 554
Leu Ala Gly Lys Val Gln Asp Ile Leu Gln Val Ser Gln Asp Glu Phe
130 135 140

cac aga atc aca aag atc aat ctc acc gct cca tgg ttt ctc ttg aag 602
His Arg Ile Thr Lys Ile Asn Leu Thr Ala Pro Trp Phe Leu Leu Lys
145 150 155

gct gta gcc aca agg atg aag gac cat gga tca gga ggc tcc att gtc 650
Ala Val Ala Thr Arg Met Lys Asp His Gly Ser Gly Gly Ser Ile Val
160 165 170

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Phe Met Ala Thr Ile Ala Ser Gly Glu Arg Ala Leu Tyr Pro Gly Ala
175 180 185

gat gcc tac gct tca act tct gcc gct att cac cag ctc gtc cgg gta 746
Asp Ala Tyr Ala Ser Thr Ser Ala Ala Ile His Gln Leu Val Arg Val
190 195 200 205

tgc atc cta gct cct aat tagacacatc gcgttcgtaa cttgaatatg 794
Cys Ile Leu Ala Pro Asn
210

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caacatgatc tctagagggc tgcattctgga tgatgagtat acagcttctg tgggaagaga 914

ccgagcgcag aagctgggtca aggacgctgc acccctcggc cagtgggtca acccggacac 974

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cactgtcttg gtggatggag cgcagtcctt tacgcgaccc cgtctcaaata cctacatgtg 1094

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<213> Arabidopsis thaliana

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35 40 45
Arg Asp Ser Ile Glu Gly Ala Phe Pro Ala Asp Val Ile Ala Leu Asp
50 55 60
Met Glu Ser Asp Ser Glu Val Ala Phe His Ala Ala Val Gln Lys Ala
65 70 75 80
Trp Glu Leu Ser Gly His Phe Asp Ala Phe Leu Asn Ser Tyr Thr Tyr
85 90 95
Gln Gly Leu Ile Cys Phe Leu Phe Phe Thr Thr Leu Pro Leu Met Leu
100 105 110
Leu Cys Val Asp His Ser Phe Ile Gln Gln Ser Phe Phe Leu Ala Gly
115 120 125
Lys Val Gln Asp Ile Leu Gln Val Ser Gln Asp Glu Phe His Arg Ile
130 135 140
Thr Lys Ile Asn Leu Thr Ala Pro Trp Phe Leu Leu Lys Ala Val Ala
145 150 155 160

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Thr Arg Met Lys Asp His Gly Ser Gly Gly Ser Ile Val Phe Met Ala
 165 170 175
 Thr Ile Ala Ser Gly Glu Arg Ala Leu Tyr Pro Gly Ala Asp Ala Tyr
 180 185 190
 Ala Ser Thr Ser Ala Ala Ile His Gln Leu Val Arg Val Cys Ile Leu
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 Ala Pro Asn
 210

<210> 13
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 <222> (1)..(1143)
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 At1g63140

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 cta atc aaa gaa gaa caa cgt tat cac gaa gat acg gtg agc ttg caa 96
 Leu Ile Lys Glu Glu Gln Arg Tyr His Glu Asp Thr Val Ser Leu Gln
 20 25 30
 gcg gag agg att ttg cat gcc atg acc ttc ccc atg gtt ctc aaa act 144
 Ala Glu Arg Ile Leu His Ala Met Thr Phe Pro Met Val Leu Lys Thr
 35 40 45
 gct ttg gag ctt ggc gtt atc gac atg atc act tct gta gat gac ggc 192
 Ala Leu Glu Leu Gly Val Ile Asp Met Ile Thr Ser Val Asp Asp Gly
 50 55 60
 gtg tgg ctc tcg cct tct gag atc gct ctt ggt ctc cca acc aag ccc 240
 Val Trp Leu Ser Pro Ser Glu Ile Ala Leu Gly Leu Pro Thr Lys Pro
 65 70 75 80
 acc aat ccg gag gca cca gta ttg ctg gac cgg atg cta gtt ttg tta 288
 Thr Asn Pro Glu Ala Pro Val Leu Leu Asp Arg Met Leu Val Leu Leu
 85 90 95
 gcc agc cac tca atc ttg aag tac cgt acg gta gaa acc gga gat aac 336
 Ala Ser His Ser Ile Leu Lys Tyr Arg Thr Val Glu Thr Gly Asp Asn
 100 105 110
 att gga agt aga aag acc gag agg gtc tat gca gct gaa ccg gtt tgc 384
 Ile Gly Ser Arg Lys Thr Glu Arg Val Tyr Ala Ala Glu Pro Val Cys
 115 120 125
 acg ttt ttc ttg aac cgc gga gat ggc ttg ggc tct ctc gcc act ttg 432
 Thr Phe Phe Leu Asn Arg Gly Asp Gly Leu Gly Ser Leu Ala Thr Leu
 130 135 140
 ttc atg gta ctc caa ggg gaa gtc tgt atg aag cct tgg gaa cat ctc 480
 Phe Met Val Leu Gln Gly Glu Val Cys Met Lys Pro Trp Glu His Leu
 145 150 155 160

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Lys Asp Met Ile Leu 165 Glu Gly Lys Asp Ala 170 Phe Thr Ser Ala 175 His Gly	
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Met Arg Phe 180 Glu Leu Ile Gly Ser 185 Asn Glu Gln Phe 190 Ala Glu Met	
ttt aac cgg gca atg tcg gaa gct tcc aca ttg att atg aag aag gtt	624
Phe Asn Arg 195 Ala Met Ser Glu Ala 200 Ser Thr Leu Ile 205 Met Lys Lys Val	
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Leu Glu Val Tyr Lys Gly Phe 215 Glu Asp Val Asn 220 Thr Leu Val Asp Val	
gga gga gga att gga aca atc ata ggt caa gtg act tcc aag tat cct	720
Gly Gly Gly Ile Gly Thr 230 Ile Ile Gly Gln Val 235 Thr Ser Lys Tyr Pro 240	
cat att aaa ggc atc aat ttc gat cta gca tcg gtt tta gcc cat gct	768
His Ile Lys Gly 245 Ile Asn Phe Asp Leu Ala 250 Ser Val Leu Ala 255 His Ala	
cct ttt aat aaa gga gtg gag cat gtt tca gga gat atg ttt aaa gaa	816
Pro Phe Asn Lys 260 Gly Val Glu His 265 Val Ser Gly Asp Met Phe 270 Lys Glu	
att cca aaa gga gat gcc atc ttc atg aaa tgg ata cta cat gat tgg	864
Ile Pro Lys 275 Gly Asp Ala Ile Phe 280 Met Lys Trp Ile 285 Leu His Asp Trp	
act gac gaa gat tgt gta aag atc cta aaa aat tat tgg aaa agt ctt	912
Thr Asp Glu Asp Cys Val Lys 295 Ile Leu Lys Asn Tyr 300 Trp Lys Ser Leu	
ccc gag aaa gga aaa gtg ata ata gtc gag gtg gtt acg ccc gag gaa	960
Pro Glu Lys Gly Lys Val 310 Ile Ile Val Glu Val 315 Val Thr Pro Glu Glu 320	
cca aag att aac gac att tct tct aac att gtg ttc ggt atg gac atg	1008
Pro Lys Ile Asn Asp 325 Ile Ser Ser Asn 330 Ile Val Phe Gly Met Asp 335 Met	
ctg atg tta gca gta agc tca ggt ggt aag gag agg tct ctt tcc caa	1056
Leu Met Leu Ala Val Ser Ser Gly 345 Gly Lys Glu Arg Ser 350 Leu Ser Gln	
ttc gag act cta gcc tct gat tcg ggt ttt ctt cgt tgt gaa atc att	1104
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<212> PRT

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<400> 14

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20 25 30

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Val	Trp	Leu	Ser	Pro	Ser	Glu	Ile	Ala	Leu	Gly	Leu	Pro	Thr	Lys	Pro
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Thr	Asn	Pro	Glu	Ala	Pro	Val	Leu	Leu	Asp	Arg	Met	Leu	Val	Leu	Leu
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Ala	Ser	His	Ser	Ile	Leu	Lys	Tyr	Arg	Thr	Val	Glu	Thr	Gly	Asp	Asn
			100					105					110		
Ile	Gly	Ser	Arg	Lys	Thr	Glu	Arg	Val	Tyr	Ala	Ala	Glu	Pro	Val	Cys
		115					120					125			
Thr	Phe	Phe	Leu	Asn	Arg	Gly	Asp	Gly	Leu	Gly	Ser	Leu	Ala	Thr	Leu
	130					135					140				
Phe	Met	Val	Leu	Gln	Gly	Glu	Val	Cys	Met	Lys	Pro	Trp	Glu	His	Leu
	145				150					155					160
Lys	Asp	Met	Ile	Leu	Glu	Gly	Lys	Asp	Ala	Phe	Thr	Ser	Ala	His	Gly
				165					170					175	
Met	Arg	Phe	Phe	Glu	Leu	Ile	Gly	Ser	Asn	Glu	Gln	Phe	Ala	Glu	Met
			180					185					190		
Phe	Asn	Arg	Ala	Met	Ser	Glu	Ala	Ser	Thr	Leu	Ile	Met	Lys	Lys	Val
		195					200					205			
Leu	Glu	Val	Tyr	Lys	Gly	Phe	Glu	Asp	Val	Asn	Thr	Leu	Val	Asp	Val
	210					215					220				
Gly	Gly	Gly	Ile	Gly	Thr	Ile	Ile	Gly	Gln	Val	Thr	Ser	Lys	Tyr	Pro
	225				230					235					240
His	Ile	Lys	Gly	Ile	Asn	Phe	Asp	Leu	Ala	Ser	Val	Leu	Ala	His	Ala
				245					250					255	
Pro	Phe	Asn	Lys	Gly	Val	Glu	His	Val	Ser	Gly	Asp	Met	Phe	Lys	Glu
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Ile	Pro	Lys	Gly	Asp	Ala	Ile	Phe	Met	Lys	Trp	Ile	Leu	His	Asp	Trp
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Thr	Asp	Glu	Asp	Cys	Val	Lys	Ile	Leu	Lys	Asn	Tyr	Trp	Lys	Ser	Leu
	290					295					300				
Pro	Glu	Lys	Gly	Lys	Val	Ile	Ile	Val	Glu	Val	Val	Thr	Pro	Glu	Glu
	305				310					315					320
Pro	Lys	Ile	Asn	Asp	Ile	Ser	Ser	Asn	Ile	Val	Phe	Gly	Met	Asp	Met
			325						330					335	
Leu	Met	Leu	Ala	Val	Ser	Ser	Gly	Gly	Lys	Glu	Arg	Ser	Leu	Ser	Gln
			340					345					350		
Phe	Glu	Thr	Leu	Ala	Ser	Asp	Ser	Gly	Phe	Leu	Arg	Cys	Glu	Ile	Ile
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Cys	His	Ala	Phe	Ser	Tyr	Ser	Val	Ile	Glu	Leu	His	Lys			
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 1 5 10 15
 cac ggt tgt cgg ttg gtg ttg atg gga aac gag gct tct cta agg agc 95
 His Gly Cys Arg Leu Val Leu Met Gly Asn Glu Ala Ser Leu Arg Ser
 20 25 30
 act gtg gac tac ata cga gtc tct gtt gat gga gcc ttc cca gtg gag 143
 Thr Val Asp Tyr Ile Arg Val Ser Val Asp Gly Ala Phe Pro Val Glu
 35 40 45
 ctc att gga gcc gac atg gaa gct gat agt gag gaa gat ttc tat gtt 191
 Leu Ile Gly Ala Asp Met Glu Ala Asp Ser Glu Glu Asp Phe Tyr Val
 50 55 60
 gct gtc caa aag gca tgg act cgt cta gga tct ttg gat gct ttt gtc 239
 Ala Val Gln Lys Ala Trp Thr Arg Leu Gly Ser Leu Asp Ala Phe Val
 65 70 75
 aac tgc tgt acc tac caa ggg aag atg cag gac att ctc cga gtg tct 287
 Asn Cys Cys Thr Tyr Gln Gly Lys Met Gln Asp Ile Leu Arg Val Ser
 80 85 90 95
 gaa gat gag ttc aag aaa atc aca agg atc aat ctc acg gct aca tgg 335
 Glu Asp Glu Phe Lys Lys Ile Thr Arg Ile Asn Leu Thr Ala Thr Trp
 100 105 110
 ttt atc ttg aag gct gtg gca agc atg atg aag gag aat gga aca gga 383
 Phe Ile Leu Lys Ala Val Ala Ser Met Met Lys Glu Asn Gly Thr Gly
 115 120 125
 ggc tcc att gg 394
 Gly Ser Ile
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<210> 16
 <211> 130
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 <213> Brassica napus

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 1 5 10 15
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 Val Asp Tyr Ile Arg Val Ser Val Asp Gly Ala Phe Pro Val Glu Leu
 35 40 45
 Ile Gly Ala Asp Met Glu Ala Asp Ser Glu Glu Asp Phe Tyr Val Ala
 50 55 60
 Val Gln Lys Ala Trp Thr Arg Leu Gly Ser Leu Asp Ala Phe Val Asn
 65 70 75 80

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Cys Cys Thr Tyr Gln Gly Lys Met Gln Asp Ile Leu Arg Val Ser Glu
85 90 95
Asp Glu Phe Lys Lys Ile Thr Arg Ile Asn Leu Thr Ala Thr Trp Phe
100 105 110
Ile Leu Lys Ala Val Ala Ser Met Met Lys Glu Asn Gly Thr Gly Gly
115 120 125
Ser Ile
130

<210> 17
<211> 429
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<213> Brassica napus
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<222> (2)..(427)
<223> coding for Brassica homologue H3

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Glu Phe Ser Gly Arg Arg Phe Arg Thr Thr Leu Asn Leu Met Ala Asn
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aag gtg ttg atg aca gac aac ggc gac cag gtt tcc cgg aac atc gct 97
Lys Val Leu Met Thr Asp Asn Gly Asp Gln Val Ser Arg Asn Ile Ala
20 25 30
atc caa cta gcc aaa cac ggt tgt cgg ttg gtg ttg atg gga aac gag 145
Ile Gln Leu Ala Lys His Gly Cys Arg Leu Val Leu Met Gly Asn Glu
35 40 45
gct tct cta agg agc act gtg gac tac ata cga ttc tct gat gat gga 193
Ala Ser Leu Arg Ser Thr Val Asp Tyr Ile Arg Phe Ser Asp Asp Gly
50 55 60
gcc ttc cca gtg gag ctc att gga gcc gac atg gaa gct gat agt gag 241
Ala Phe Pro Val Glu Leu Ile Gly Ala Asp Met Glu Ala Asp Ser Glu
65 70 75 80
gaa gat ttc tat gtt gct gtc caa acg gca tgg act cgt cta gga tct 289
Glu Asp Phe Tyr Val Ala Val Gln Thr Ala Trp Thr Arg Leu Gly Ser
85 90 95
ttg gat gct ttt gtc aac tgc tgt acc tac caa ggg aag atg cag gac 337
Leu Asp Ala Phe Val Asn Cys Cys Thr Tyr Gln Gly Lys Met Gln Asp
100 105 110
att ctc cga gtg tct gaa gat gag ttc aag aaa atc aca cgg atc aat 385
Ile Leu Arg Val Ser Glu Asp Glu Phe Lys Lys Ile Thr Arg Ile Asn
115 120 125
ctc acg gct aca tgg ttt atc ttg aag gct gtg gca agc atg at 429
Leu Thr Ala Thr Trp Phe Ile Leu Lys Ala Val Ala Ser Met
130 135 140

<210> 18
<211> 142
<212> PRT
<213> Brassica napus

<400> 18

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			20					25					30			
Ile	Gln	Leu	Ala	Lys	His	Gly	Cys	Arg	Leu	Val	Leu	Met	Gly	Asn	Glu	
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Ala	Ser	Leu	Arg	Ser	Thr	Val	Asp	Tyr	Ile	Arg	Phe	Ser	Asp	Asp	Gly	
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Glu	Asp	Phe	Tyr	Val	Ala	Val	Gln	Thr	Ala	Trp	Thr	Arg	Leu	Gly	Ser	
			85						90					95		
Leu	Asp	Ala	Phe	Val	Asn	Cys	Cys	Thr	Tyr	Gln	Gly	Lys	Met	Gln	Asp	
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Ile	Leu	Arg	Val	Ser	Glu	Asp	Glu	Phe	Lys	Lys	Ile	Thr	Arg	Ile	Asn	
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<211> 436

<212> DNA

<213> Brassica napus

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<222> (3)..(419)

<223> coding for Brassica homologue H4

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	1				5					10				15		
gta	tat	gca	gcc	gag	ccg	ggt	tgc	acg	ctt	ttc	tta	aaa	cat	ggt	cat	95
Val	Tyr	Ala	Ala	Glu	Pro	Val	Cys	Thr	Leu	Phe	Leu	Lys	His	Gly	His	
			20					25						30		
gag	tcg	ggt	tca	ctc	atg	tcc	cta	ttc	atg	gtg	cac	cat	agc	caa	gtc	143
Glu	Ser	Gly	Ser	Leu	Met	Ser	Leu	Phe	Met	Val	His	His	Ser	Gln	Val	
			35					40					45			
ttt	ttc	gaa	act	tggt	aca	cat	ttg	aaa	gat	ctg	ata	caa	gaa	gga	aaa	191
Phe	Phe	Glu	Thr	Trp	Thr	His	Leu	Lys	Asp	Leu	Ile	Gln	Glu	Gly	Lys	
		50					55					60				
gat	aca	ttc	att	tct	gct	cat	ggc	atg	agg	atc	ttt	gaa	tac	atc	ggt	239
Asp	Thr	Phe	Ile	Ser	Ala	His	Gly	Met	Arg	Ile	Phe	Glu	Tyr	Ile	Gly	
	65					70					75					
ttg	aat	gaa	caa	ttc	gct	tgt	atg	ttt	aac	cat	gca	atg	tca	gaa	tct	287
Leu	Asn	Glu	Gln	Phe	Ala	Cys	Met	Phe	Asn	His	Ala	Met	Ser	Glu	Ser	
	80				85				90					95		
tct	acc	atg	atc	atg	aag	aag	att	tta	gaa	gtt	tac	aga	gga	ttc	gaa	335
Ser	Thr	Met	Ile	Met	Lys	Lys	Ile	Leu	Glu	Val	Tyr	Arg	Gly	Phe	Glu	
				100					105					110		

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gat att aaa act ttg gtg gat att gga gga gga ctt ggc acc aca cta 383
Asp Ile Lys Thr Leu Val Asp Ile Gly Gly Gly Leu Gly Thr Thr Leu
115 120 125

aat ctg gtt act tcc aag tat cct cat ata agg gta taatttcgat 429
Asn Leu Val Thr Ser Lys Tyr Pro His Ile Arg Val
130 135

taaactc 436

<210> 20

<211> 139

<212> PRT

<213> Brassica napus

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20 25 30
Ser Gly Ser Leu Met Ser Leu Phe Met Val His His Ser Gln Val Phe
35 40 45
Phe Glu Thr Trp Thr His Leu Lys Asp Leu Ile Gln Glu Gly Lys Asp
50 55 60
Thr Phe Ile Ser Ala His Gly Met Arg Ile Phe Glu Tyr Ile Gly Leu
65 70 75 80
Asn Glu Gln Phe Ala Cys Met Phe Asn His Ala Met Ser Glu Ser Ser
85 90 95
Thr Met Ile Met Lys Lys Ile Leu Glu Val Tyr Arg Gly Phe Glu Asp
100 105 110
Ile Lys Thr Leu Val Asp Ile Gly Gly Gly Leu Gly Thr Thr Leu Asn
115 120 125
Leu Val Thr Ser Lys Tyr Pro His Ile Arg Val
130 135

<210> 21

<211> 418

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(417)

<223> coding for Brassica homologue H5

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act cac aag tcc ctc ttc atg ttg ctc aat agc caa gta ttt ttc aag 96
Thr His Lys Ser Leu Phe Met Leu Leu Asn Ser Gln Val Phe Phe Lys
20 25 30
aca tgg gat aat ctg aag ggt gtg ata caa gaa gga aaa gat gcg ttt 144
Thr Trp Asp Asn Leu Lys Gly Val Ile Gln Glu Gly Lys Asp Ala Phe
35 40 45

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agt tca gct cat ggc atg cca tta ttc gaa tac atc ggt ttg gat gag	192
Ser Ser Ala His Gly Met Pro Leu Phe Glu Tyr Ile Gly Leu Asp Glu	
50 55 60	
caa ttc gct ggt atg ttt aac cat gca atg gca gaa tct tct acc atc	240
Gln Phe Ala Gly Met Phe Asn His Ala Met Ala Glu Ser Ser Thr Ile	
65 70 75 80	
att atg aag aaa att tta gaa gtt tac aga gga ttc gaa gat gta aat	288
Ile Met Lys Lys Ile Leu Glu Val Tyr Arg Gly Phe Glu Asp Val Asn	
85 90 95	
act ttg gtg gat att gga gga gga ctt ggc acc gta cta aac ctt gtc	336
Thr Leu Val Asp Ile Gly Gly Gly Leu Gly Thr Val Leu Asn Leu Val	
100 105 110	
act tcc aag tat cct caa att aag ggt atc aat ttc gat tta acc atg	384
Thr Ser Lys Tyr Pro Gln Ile Lys Gly Ile Asn Phe Asp Leu Thr Met	
115 120 125	
gtt tta gcc aat gct cct tct tat cca gga gtg g	418
Val Leu Ala Asn Ala Pro Ser Tyr Pro Gly Val	
130 135	

<210> 22
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 <213> Brassica napus

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Thr Trp Asp Asn Leu Lys Gly Val Ile Gln Glu Gly Lys Asp Ala Phe	
35 40 45	
Ser Ser Ala His Gly Met Pro Leu Phe Glu Tyr Ile Gly Leu Asp Glu	
50 55 60	
Gln Phe Ala Gly Met Phe Asn His Ala Met Ala Glu Ser Ser Thr Ile	
65 70 75 80	
Ile Met Lys Lys Ile Leu Glu Val Tyr Arg Gly Phe Glu Asp Val Asn	
85 90 95	
Thr Leu Val Asp Ile Gly Gly Gly Leu Gly Thr Val Leu Asn Leu Val	
100 105 110	
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115 120 125	
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130 135	

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 <222> (4)
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<210> 24
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<220>
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 <223> R/K-variation

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<400> 25
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<400> 26
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Phe

<210> 27
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<400> 27

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Ala

<210> 28

<211> 9

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<210> 29

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<212> PRT

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<210> 31

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<222> (8)
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 <400> 31
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<210> 32
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 <223> Description of the artificial sequence: oligonucleotide primer

<400> 33
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21

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<400> 34
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21

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19

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oligonucleotide primer

<400> 36
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SEQUENCE LISTING

DT06 Rec'd PCT/PTO 0 2 MAR 2005

<110> Klebsattel, Martin
 Keetman, Ulrich
 Herbers, Karin
 Flachmann, Ralf
 Sauer, Matt
 Hillebrand, Heike

<120> Transgenic expression cassettes for expressing nucleic acids in
 nonreproductive floral tissues of plants

<130> 13173-00009-US

<150> PCT/EP 2003/009594

<151> 2003-08-29

<150> DE 102 41 124.7

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<160> 36

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<223> 76L promoter (including 5'-untranslated region) of
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tttgttccga gtgttttcgt atatgcttta aacaagcagc tactatcagc aatagcaaaa 660
gtaacatgat atttgttaat cccgttgga attcatgtcc attattttgt atatatatat 720
attatataat agtagaattt ggttatgtag tgcatttctt cttaatctat gctttctaag 780
gttaaaaaaca ggcgcccata tggacgacat aaatgtcgat atttaagagg cactgcaagt 840
tgaacaaaaa aaaaaaagta taggcactgc aaaagttatc caacgtattt aagactaagg 900
actaaagatt caaagataat attcagaaaa agaaaaagaa aaaaagagaa gataatattc 960
ggaaacatcc acaagcattc taaatctaga aaacataaat aatacagcaa agatggggat 1020
gaagatatga tccaactcca tcacagattc tcaagacaga tttagaaaagt gtcaagctca 1080
ccaaaagggg tataggagac tgactgttaa ttgaaatgct ttctacacgt ggacgcactg 1140
atatcatatt aaaacctgat tgtttgttga acattcacta actcatacca aacggtccaa 1200
acctatgtct ccattttctt aaatgttgat ttcgattcca tacctacttt gcatacatta 1260
ttgaatgtgt ttcttaagtt gtgattaaaa ttaaagtggc acaatatcac agtcgaatgg 1320
tatatcgatg taacacttta ggattgaatc aatatgaaaa gttatacacc gaatttgtga 1380
gaaacgagta tagcttagac aaaatttggt tttcttaaat taagcggaaa aataattaaa 1440
cagagaccaa attaagcgtt cttcttgaac tgaaatcact aaagtaaagt taaccggtta 1500
gtagagtgtt aactatttaa acaaagaaaa ctccaaaccc aattgagaaa ctactcaaac 1560
atagaacaaa cacataatga ttcagtagct accaatatca tattcaactt tgtttcgatt 1620
cctttaaaaa aaaatataat taaccaataa aaataggtca taatcgattc agaaacaatt 1680
tcatattctt ctctagttaa gttcagtttc attctaccgg agttgtatac aatctataat 1740
tttatcgctt attaccttaa aagcgtcctc aaaccaacca aaacaaaaat agttgcatca 1800
atgaatccat caaagcatat aaattcacac cgtcttaaaa tggagtgttg atggataagt 1860
accaacaatt ttagaccatt cacactgaat gagtatgact aacattcaca ttcacattca 1920
attaggaaag ttgtactaat gaacacacaa taaaagttaa acaaatctc tacatattct 1980
tgtacaccaa tctatattag atgatcattt taaatataca cgaatattaa ttttataaat 2040
gaaaaatcac tgcccatatt ttaattaatt tatatattta gctatcaaat attaggcata 2100

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atgttggtga ggtttctgag tataaaaaat gacaaagtat gaataccatc tataccttta 2160
ttacctatct ttctcgattt 2180

<210> 3

<211> 1033

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> promoter

<222> (1)..(1033)

<223> 76S promoter (including 5'-untranslated region) of
gene locus At3g01980

<400> 3

aggtgcatga ccaagtaaca atttgattcc tttccagcat aacgtcatgt tggttgcaaa 60
aagaaggcaa agtagagcaa gcaagcaagc aaagcatttt tcttatttta tattttgttg 120
cggattccac caccacttg aaaaattgac atgtcacaaat gatttcgtat cctagtcttt 180
tattatttaa cactctcaca atcccattac tctacacctc tttcattaag tcaacacacg 240
gttttcaaaa atccactacc ctcccaccac ctagaatctt ttgttaccta ccaacaccct 300
cctttgttct ctttatatat tgggtccaact aaatcaataa gggaaagcat ccttttggtt 360
ggaggaattg ctttcattct cactctttgt gtgttgatca atggactagc taataacaag 420
ttcctcctct atatatattca aaagaatgga acagaaacat aaacgaaaga cagagtacct 480
gatgttgatg attcattgtc tgtctggagc tcccaaagtc cttttatgct tacatattca 540
taaccaacaa cggctattaa ttataaacca aaaacacgaa ataagtttgt agcaaagtga 600
aattaggaat cttggagatg gatccattag tagtaggata ataggatatg atggaatttg 660
gttggggaac agtgataact tacgcttgct tccggcgccg ggaaagtggg aaaacctaca 720
aagtacagaa atggatctgg gccttgaagt gggcttttta ttaaagaaaa aaatacatct 780
ccgttatcaa tcaccatctt cttctatcta caaattaaag aaggtaacaa cagaacgtgg 840
tggatcatgt ggtaggcat taattatttg ctttgtttcg ccgttttggt aacacacaga 900
cacagttccg gtaagagctt ttgcagccac tctttatagt tatttagaat tggcgatcga 960
atcaatctca ctccctccct cccttaagtc ttgttgaatc tgctgaattg ttttataaag 1020
agttactttg gca 1033

<210> 4

<211> 1097

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> promoter

<222> (1)..(1097)

<223> 84S promoter (including 5'-untranslated region) of
gene locus At1g63140

<400> 4

aaagggttat aggagactga ctgttaattg aaatgctttc tacacgtgga cgcactgata 60
tcatattaaa acctgattgt ttgttgaaca ttcactaact cataccaaac ggtccaaacc 120
tatgtctcca ttttcttaaa tggtgatttc gattccatac ctactttgca tacattattg 180
aatgtgtttc ttaagttgtg attaaaatta aatgagcaca atatcacagt cgaatgggat 240
atcgatgtaa cacttttaga ttgaatcaat atgaaaagtt atacaccgaa tttgtgagaa 300
acgagtatag cttagacaaa atttgttttt cttaaattaa gcggaaaaat aattaaacag 360
agaccaaatt aagcgttctt cttgaactga aatcactaaa gtaaagttaa cccgttagta 420
gagtgttaac tatttaacaa aagaaaactc caaacccaat tgagaaacta ctcaaacata 480
gaaacaacac ataattgatt agtagctacc aatatcatat tcaactttgt ttcgattcct 540
ttaaaacaaa atataattaa ccaaataaaa taggtcataa tcgattcaga aacaatttca 600
tattcttctc tagtttagtt cagtttcatt ctaccggagt tgtatacaat ctataatttt 660
atcgcttatt accttaaaag cgtcctcaaa ccaacaaaaa caaaaatagt tgcattcaat 720
aatccatcaa agcatataaa ttcacaccgt tctaaaatgg agtggtgatg gataagtacc 780
aacaatttta gaccattcac actgaatgag tatgactaac attcacattc acattcaatt 840

```

aggaaagttg tactaatgaa cacacaataa aagtgaaaac aaatctctac atattcttgt 900
acaccaatct atattagatg atcattttta atatacacga atattaattt tataaatgaa 960
aaatacgtgc ccatatttta attaatattat atatttagct atcaaattt aggcataatg 1020
ttggtgaggt ttctgagtat aaaaaatgac aaagtatgaa taccatctat acctttatta 1080
cctatctttc tcgattt                                     1097

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```

<210> 5
<211> 19
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> Description of the artificial sequence:
      Oligonucleotide primer

```

```

<400> 5
gaccctgtcc cacctccaa                                     19

```

```

<210> 6
<211> 21
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> Description of the artificial sequence:
      Oligonucleotide primer

```

```

<400> 6
tgagaactgc gattgtttgc a                                   21

```

```

<210> 7
<211> 25
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> Description of the artificial sequence:
      Oligonucleotide primer

```

```

<400> 7
gtcgactatc ctctgcgcaa tgaat                               25

```

```

<210> 8
<211> 25
<212> DNA
<213> Artificial sequence

```

```

<220>
<223> Description of the artificial sequence:
      Oligonucleotide primer

```

```

<400> 8
cccgggaaat cgagaaagat aggta                               25

```

```

<210> 9

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<211> 25
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence:
 Oligonucleotide primer

<400> 9

gtcgacaaag gggttatagga gactg 25

<210> 10

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:
 Oligonucleotide primer

<400> 10

gtcgaccatg tttcagagga tatgt 25

<210> 11

<211> 1187

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (132)..(764)

<223> coding for gene product of Arabidopsis thaliana
 gene locus At3g01980

<400> 11

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gttcggttaa gagcttttgc agccactctt tatagttatt tagaattggc gatcgaatca 60
atctcactcc ctccctccct taagtcttgt tgaatctgct gaattgtttt ataaagagtt 120
actttggcaa a atg gaa aat ccg gcg aag aga gtg ttg atg aca tcc aac 170
          Met Glu Asn Pro Ala Lys Arg Val Leu Met Thr Ser Asn
          1              5              10
ggc gac gag gtg tcc cga aac atc gct ttc cat cta gcc aaa cac ggt 218
Gly Asp Glu Val Ser Arg Asn Ile Ala Phe His Leu Ala Lys His Gly
          15              20              25
tgc aag ttg gta atg atg gga aat gag ggt tcc cta agg agc att gta 266
Cys Lys Leu Val Met Met Gly Asn Glu Gly Ser Leu Arg Ser Ile Val
          30              35              40              45
gac aag att aga gat tcc att gag gga gcc ttc cct gcc gat gtt ata 314
Asp Lys Ile Arg Asp Ser Ile Glu Gly Ala Phe Pro Ala Asp Val Ile
          50              55              60
gca ctc gac atg gaa tct gac tct gaa gtt gct ttt cat gcc gct gtc 362
Ala Leu Asp Met Glu Ser Asp Ser Glu Val Ala Phe His Ala Ala Val
          65              70              75
caa aag gca tgg gaa ctt tcc ggc cat ttc gat gct ttt ctc aac tct 410
Gln Lys Ala Trp Glu Leu Ser Gly His Phe Asp Ala Phe Leu Asn Ser
          80              85              90
tat acc tac caa ggt tta att tgc ttc ttg ttt ttc act acc ctg cct 458
Tyr Thr Tyr Gln Gly Leu Ile Cys Phe Leu Phe Phe Thr Thr Leu Pro
          95              100              105

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ttg atg ctc ttg tgt gtt gat cat tcc ttt att caa caa tct ttc ttt 506
Leu Met Leu Leu Cys Val Asp His Ser Phe Ile Gln Gln Ser Phe Phe
110 115 120 125
ctt gca gga aag gtg cag gac att ctt caa gtc tct caa gat gag ttc 554
Leu Ala Gly Lys Val Gln Asp Ile Leu Gln Val Ser Gln Asp Glu Phe
130 135 140
cac aga atc aca aag atc aat ctc acc gct cca tgg ttt ctc ttg aag 602
His Arg Ile Thr Lys Ile Asn Leu Thr Ala Pro Trp Phe Leu Leu Lys
145 150 155
gct gta gcc aca agg atg aag gac cat gga tca gga ggc tcc att gtc 650
Ala Val Ala Thr Arg Met Lys Asp His Gly Ser Gly Gly Ser Ile Val
160 165 170
ttc atg gcc act atc gcc agc gga gag agg gcg ctt tac cct ggc gct 698
Phe Met Ala Thr Ile Ala Ser Gly Glu Arg Ala Leu Tyr Pro Gly Ala
175 180 185
gat gcc tac gct tca act tct gcc gct att cac cag ctc gtc cgg gta 746
Asp Ala Tyr Ala Ser Thr Ser Ala Ala Ile His Gln Leu Val Arg Val
190 195 200 205
tgc atc cta gct cct aat tagacacatc gcgttcgtaa cttgaatatg 794
Cys Ile Leu Ala Pro Asn
210
tttgttgatg attgggtttc aggcattcagc catgagtctc gggaagcaca agatacgggt 854
caacatgatac tctagagggc tgcattctgga tgatgagtat acagcttctg tgggaagaga 914
ccgagcgcagc aagctggta aggacgtgc acccctcggc cagtggctca acccgacac 974
agacctctac tccactgtta tctacttgat cagcgatggc tcacgcttca tgacaggcac 1034
cactgtcttg gtggatggag cgcagtcctt tacgcgaccc cgtctcaaata cctacatgtg 1094
atcaatgcct agtattatta taattctatg ttgtgtgtaa aaagtgaata tgaatcaagt 1154
ttgaataact atggagggat gaataatcca tcc 1187

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<210> 12

<211> 211

<212> PRT

<213> Arabidopsis thaliana

<400> 12

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Met Glu Asn Pro Ala Lys Arg Val Leu Met Thr Ser Asn Gly Asp Glu
1 5 10 15
Val Ser Arg Asn Ile Ala Phe His Leu Ala Lys His Gly Cys Lys Leu
20 25 30
Val Met Met Gly Asn Glu Gly Ser Leu Arg Ser Ile Val Asp Lys Ile
35 40 45
Arg Asp Ser Ile Glu Gly Ala Phe Pro Ala Asp Val Ile Ala Leu Asp
50 55 60
Met Glu Ser Asp Ser Glu Val Ala Phe His Ala Ala Val Gln Lys Ala
65 70 75 80
Trp Glu Leu Ser Gly His Phe Asp Ala Phe Leu Asn Ser Tyr Thr Tyr
85 90 95
Gln Gly Leu Ile Cys Phe Leu Phe Phe Thr Thr Leu Pro Leu Met Leu
100 105 110
Leu Cys Val Asp His Ser Phe Ile Gln Gln Ser Phe Phe Leu Ala Gly
115 120 125
Lys Val Gln Asp Ile Leu Gln Val Ser Gln Asp Glu Phe His Arg Ile
130 135 140
Thr Lys Ile Asn Leu Thr Ala Pro Trp Phe Leu Leu Lys Ala Val Ala
145 150 155 160
Thr Arg Met Lys Asp His Gly Ser Gly Gly Ser Ile Val Phe Met Ala
165 170 175
Thr Ile Ala Ser Gly Glu Arg Ala Leu Tyr Pro Gly Ala Asp Ala Tyr
180 185 190

```


Ala Ser Thr Ser Ala Ala Ile His Gln Leu Val Arg Val Cys Ile Leu
 195 200 205
 Ala Pro Asn
 210

<210> 13
 <211> 1146
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(1143)
 <223> coding for transcript (cDNA) of gene locus
 At1g63140

<400> 13
 atg gag aac cat ctt caa cat tcc tta acc atc att cct aaa ccg gat 48
 Met Glu Asn His Leu Gln His Ser Leu Thr Ile Ile Pro Lys Pro Asp
 1 5 10 15
 cta atc aaa gaa gaa caa cgt tat cac gaa gat acg gtg agc ttg caa 96
 Leu Ile Lys Glu Gln Arg Tyr His Glu Asp Thr Val Ser Leu Gln
 20 25 30
 gcg gag agg att ttg cat gcc atg acc ttc ccc atg gtt ctc aaa act 144
 Ala Glu Arg Ile Leu His Ala Met Thr Phe Pro Met Val Leu Lys Thr
 35 40 45
 gct ttg gag ctt ggc gtt atc gac atg atc act tct gta gat gac ggc 192
 Ala Leu Glu Leu Gly Val Ile Asp Met Ile Thr Ser Val Asp Asp Gly
 50 55 60
 gtg tgg ctc tcg cct tct gag atc gct ctt ggt ctc cca acc aag ccc 240
 Val Trp Leu Ser Pro Ser Glu Ile Ala Leu Gly Leu Pro Thr Lys Pro
 65 70 75 80
 acc aat ccg gag gca cca gta ttg ctg gac cgg atg cta gtt ttg tta 288
 Thr Asn Pro Glu Ala Pro Val Leu Leu Asp Arg Met Leu Val Leu Leu
 85 90 95
 gcc agc cac tca atc ttg aag tac cgt acg gta gaa acc gga gat aac 336
 Ala Ser His Ser Ile Leu Lys Tyr Arg Thr Val Glu Thr Gly Asp Asn
 100 105 110
 att gga agt aga aag acc gag agg gtc tat gca gct gaa ccg gtt tgc 384
 Ile Gly Ser Arg Lys Thr Glu Arg Val Tyr Ala Ala Glu Pro Val Cys
 115 120 125
 acg ttt ttc ttg aac cgc gga gat ggc ttg ggc tct ctc gcc act ttg 432
 Thr Phe Phe Leu Asn Arg Gly Asp Gly Leu Gly Ser Leu Ala Thr Leu
 130 135 140
 ttc atg gta ctc caa ggg gaa gtc tgt atg aag cct tgg gaa cat ctc 480
 Phe Met Val Leu Gln Gly Glu Val Cys Met Lys Pro Trp Glu His Leu
 145 150 155 160
 aaa gac atg ata tta gaa gga aaa gat gca ttc acc tct gct cat ggc 528
 Lys Asp Met Ile Leu Glu Gly Lys Asp Ala Phe Thr Ser Ala His Gly
 165 170 175
 atg agg ttt ttc gaa ctc att ggt tcg aac gaa caa ttc gct gaa atg 576
 Met Arg Phe Phe Glu Leu Ile Gly Ser Asn Glu Gln Phe Ala Glu Met
 180 185 190
 ttt aac cgg gca atg tcg gaa gct tcc aca ttg att atg aag aag gtt 624
 Phe Asn Arg Ala Met Ser Glu Ala Ser Thr Leu Ile Met Lys Lys Val
 195 200 205
 tta gaa gtt tac aaa gga ttc gaa gat gta aat act ttg gtg gat gtg 672
 Leu Glu Val Tyr Lys Gly Phe Glu Asp Val Asn Thr Leu Val Asp Val
 210 215 220

gga gga gga att gga aca atc ata ggt caa gtg act tcc aag tat cct	720
Gly Gly Gly Ile Gly Thr Ile Ile Gly Gln Val Thr Ser Lys Tyr Pro	
225 230 235 240	
cat att aaa ggc atc aat ttc gat cta gca tcg gtt tta gcc cat gct	768
His Ile Lys Gly Ile Asn Phe Asp Leu Ala Ser Val Leu Ala His Ala	
245 250 255	
cct ttt aat aaa gga gtg gag cat gtt tca gga gat atg ttt aaa gaa	816
Pro Phe Asn Lys Gly Val Glu His Val Ser Gly Asp Met Phe Lys Glu	
260 265 270	
att cca aaa gga gat gcc atc ttc atg aaa tgg ata cta cat gat tgg	864
Ile Pro Lys Gly Asp Ala Ile Phe Met Lys Trp Ile Leu His Asp Trp	
275 280 285	
act gac gaa gat tgt gta aag atc cta aaa aat tat tgg aaa agt ctt	912
Thr Asp Glu Asp Cys Val Lys Ile Leu Lys Asn Tyr Trp Lys Ser Leu	
290 295 300	
ccc gag aaa gga aaa gtg ata ata gtc gag gtg gtt acg ccc gag gaa	960
Pro Glu Lys Gly Lys Val Ile Ile Val Glu Val Val Thr Pro Glu Glu	
305 310 315 320	
cca aag att aac gac att tct tct aac att gtg ttc ggt atg gac atg	1008.
Pro Lys Ile Asn Asp Ile Ser Ser Asn Ile Val Phe Gly Met Asp Met	
325 330 335	
ctg atg tta gca gta agc tca ggt ggt aag gag agg tct ctt tcc caa	1056
Leu Met Leu Ala Val Ser Ser Gly Lys Glu Arg Ser Leu Ser Gln	
340 345 350	
ttc gag act cta gcc tct gat tcg ggt ttt ctt cgt tgt gaa atc att	1104
Phe Glu Thr Leu Ala Ser Asp Ser Gly Phe Leu Arg Cys Glu Ile Ile	
355 360 365	
tgt cat gcc ttc tca tat agt gtt atc gaa tta cac aaa tag	1146
Cys His Ala Phe Ser Tyr Ser Val Ile Glu Leu His Lys	
370 375 380	

<210> 14

<211> 381

<212> PRT

<213> Arabidopsis thaliana

<400> 14

Met Glu Asn His Leu Gln His Ser Leu Thr Ile Ile Pro Lys Pro Asp	
1 5 10 15	
Leu Ile Lys Glu Glu Gln Arg Tyr His Glu Asp Thr Val Ser Leu Gln	
20 25 30	
Ala Glu Arg Ile Leu His Ala Met Thr Phe Pro Met Val Leu Lys Thr	
35 40 45	
Ala Leu Glu Leu Gly Val Ile Asp Met Ile Thr Ser Val Asp Asp Gly	
50 55 60	
Val Trp Leu Ser Pro Ser Glu Ile Ala Leu Gly Leu Pro Thr Lys Pro	
65 70 75 80	
Thr Asn Pro Glu Ala Pro Val Leu Leu Asp Arg Met Leu Val Leu Leu	
85 90 95	
Ala Ser His Ser Ile Leu Lys Tyr Arg Thr Val Glu Thr Gly Asp Asn	
100 105 110	
Ile Gly Ser Arg Lys Thr Glu Arg Val Tyr Ala Ala Glu Pro Val Cys	
115 120 125	
Thr Phe Phe Leu Asn Arg Gly Asp Gly Leu Gly Ser Leu Ala Thr Leu	
130 135 140	
Phe Met Val Leu Gln Gly Glu Val Cys Met Lys Pro Trp Glu His Leu	
145 150 155 160	
Lys Asp Met Ile Leu Glu Gly Lys Asp Ala Phe Thr Ser Ala His Gly	
165 170 175	

Met	Arg	Phe	Phe	Glu	Leu	Ile	Gly	Ser	Asn	Glu	Gln	Phe	Ala	Glu	Met
			180					185					190		
Phe	Asn	Arg	Ala	Met	Ser	Glu	Ala	Ser	Thr	Leu	Ile	Met	Lys	Lys	Val
		195					200					205			
Leu	Glu	Val	Tyr	Lys	Gly	Phe	Glu	Asp	Val	Asn	Thr	Leu	Val	Asp	Val
		210				215					220				
Gly	Gly	Gly	Ile	Gly	Thr	Ile	Ile	Gly	Gln	Val	Thr	Ser	Lys	Tyr	Pro
225					230					235					240
His	Ile	Lys	Gly	Ile	Asn	Phe	Asp	Leu	Ala	Ser	Val	Leu	Ala	His	Ala
			245						250					255	
Pro	Phe	Asn	Lys	Gly	Val	Glu	His	Val	Ser	Gly	Asp	Met	Phe	Lys	Glu
			260					265					270		
Ile	Pro	Lys	Gly	Asp	Ala	Ile	Phe	Met	Lys	Trp	Ile	Leu	His	Asp	Trp
		275					280					285			
Thr	Asp	Glu	Asp	Cys	Val	Lys	Ile	Leu	Lys	Asn	Tyr	Trp	Lys	Ser	Leu
		290				295					300				
Pro	Glu	Lys	Gly	Lys	Val	Ile	Ile	Val	Glu	Val	Val	Thr	Pro	Glu	Glu
305					310				315						320
Pro	Lys	Ile	Asn	Asp	Ile	Ser	Ser	Asn	Ile	Val	Phe	Gly	Met	Asp	Met
			325					330						335	
Leu	Met	Leu	Ala	Val	Ser	Ser	Gly	Gly	Lys	Glu	Arg	Ser	Leu	Ser	Gln
			340				345						350		
Phe	Glu	Thr	Leu	Ala	Ser	Asp	Ser	Gly	Phe	Leu	Arg	Cys	Glu	Ile	Ile
		355				360						365			
Cys	His	Ala	Phe	Ser	Tyr	Ser	Val	Ile	Glu	Leu	His	Lys			
	370					375					380				

<210> 15
 <211> 394
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (3)..(392)
 <223> coding for Brassica homologue H2

<400> 15

cc aac ggc gac gag gtt tcc cgg aac atc gct atc caa cta gcc aaa	47
Asn Gly Asp Glu Val Ser Arg Asn Ile Ala Ile Gln Leu Ala Lys	
1 5 10 15	
cac ggt tgt cgg ttg gtg ttg atg gga aac gag gct tct cta agg agc	95
His Gly Cys Arg Leu Val Leu Met Gly Asn Glu Ala Ser Leu Arg Ser	
20 25 30	
act gtg gac tac ata cga gtc tct gtt gat gga gcc ttc cca gtg gag	143
Thr Val Asp Tyr Ile Arg Val Ser Val Asp Gly Ala Phe Pro Val Glu	
35 40 45	
ctc att gga gcc gac atg gaa gct gat agt gag gaa gat ttc tat gtt	191
Leu Ile Gly Ala Asp Met Glu Ala Asp Ser Glu Glu Asp Phe Tyr Val	
50 55 60	
gct gtc caa aag gca tgg act cgt cta gga tct ttg gat gct ttt gtc	239
Ala Val Gln Lys Ala Trp Thr Arg Leu Gly Ser Leu Asp Ala Phe Val	
65 70 75	
aac tgc tgt acc tac caa ggg aag atg cag gac att ctc cga gtg tct	287
Asn Cys Cys Thr Tyr Gln Gly Lys Met Gln Asp Ile Leu Arg Val Ser	
80 85 90 95	
gaa gat gag ttc aag aaa atc aca agg atc aat ctc acg gct aca tgg	335
Glu Asp Glu Phe Lys Ile Thr Arg Ile Asn Leu Thr Ala Thr Trp	
100 105 110	

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ttt atc ttg aag gct gtg gca agc atg atg aag gag aat gga aca gga 383
Phe Ile Leu Lys Ala Val Ala Ser Met Met Lys Glu Asn Gly Thr Gly
      115                      120                      125
ggc tcc att gg 394
Gly Ser Ile
      130

```

```

<210> 16
<211> 130
<212> PRT
<213> Brassica napus

```

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<400> 16
Asn Gly Asp Glu Val Ser Arg Asn Ile Ala Ile Gln Leu Ala Lys His
 1          5          10          15
Gly Cys Arg Leu Val Leu Met Gly Asn Glu Ala Ser Leu Arg Ser Thr
      20          25          30
Val Asp Tyr Ile Arg Val Ser Val Asp Gly Ala Phe Pro Val Glu Leu
      35          40          45
Ile Gly Ala Asp Met Glu Ala Asp Ser Glu Glu Asp Phe Tyr Val Ala
      50          55          60
Val Gln Lys Ala Trp Thr Arg Leu Gly Ser Leu Asp Ala Phe Val Asn
      65          70          75          80
Cys Cys Thr Tyr Gln Gly Lys Met Gln Asp Ile Leu Arg Val Ser Glu
      85          90          95
Asp Glu Phe Lys Lys Ile Thr Arg Ile Asn Leu Thr Ala Thr Trp Phe
      100          105          110
Ile Leu Lys Ala Val Ala Ser Met Met Lys Glu Asn Gly Thr Gly Gly
      115          120          125
Ser Ile
      130

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```

<210> 17
<211> 429
<212> DNA
<213> Brassica napus

```

```

<220>
<221> CDS
<222> (2)..(427)
<223> coding for Brassica homologue H3

```

```

<400> 17
g gaa ttt tcg ggt cga cga ttt cgt act act ctg aat cta atg gcc aat 49
  Glu Phe Ser Gly Arg Arg Phe Arg Thr Thr Leu Asn Leu Met Ala Asn
  1          5          10          15
aag gtg ttg atg aca gac aac ggc gac cag gtt tcc cgg aac atc gct 97
Lys Val Leu Met Thr Asp Asn Gly Asp Gln Val Ser Arg Asn Ile Ala
      20          25          30
atc caa cta gcc aaa cac ggt tgt cgg ttg gtg ttg atg gga aac gag 145
Ile Gln Leu Ala Lys His Gly Cys Arg Leu Val Leu Met Gly Asn Glu
      35          40          45
gct tct cta agg agc act gtg gac tac ata cga ttc tct gat gat gga 193
Ala Ser Leu Arg Ser Thr Val Asp Tyr Ile Arg Phe Ser Asp Asp Gly
      50          55          60
gcc ttc cca gtg gag ctc att gga gcc gac atg gaa gct gat agt gag 241
Ala Phe Pro Val Glu Leu Ile Gly Ala Asp Met Glu Ala Asp Ser Glu
      65          70          75          80

```

```

gaa gat ttc tat gtt gct gtc caa acg gca tgg act cgt cta gga tct 289
Glu Asp Phe Tyr Val Ala Val Gln Thr Ala Trp Thr Arg Leu Gly Ser
      85      90      95
ttg gat gct ttt gtc aac tgc tgt acc tac caa ggg aag atg cag gac 337
Leu Asp Ala Phe Val Asn Cys Cys Thr Tyr Gln Gly Lys Met Gln Asp
      100      105      110
att ctc cga gtg tct gaa gat gag ttc aag aaa atc aca cgg atc aat 385
Ile Leu Arg Val Ser Glu Asp Glu Phe Lys Lys Ile Thr Arg Ile Asn
      115      120      125
ctc acg gct aca tgg ttt atc ttg aag gct gtg gca agc atg at 429
Leu Thr Ala Thr Trp Phe Ile Leu Lys Ala Val Ala Ser Met
      130      135      140

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<210> 18
 <211> 142
 <212> PRT
 <213> Brassica napus

```

<400> 18
Glu Phe Ser Gly Arg Arg Phe Arg Thr Thr Leu Asn Leu Met Ala Asn
 1      5      10      15
Lys Val Leu Met Thr Asp Asn Gly Asp Gln Val Ser Arg Asn Ile Ala
      20      25      30
Ile Gln Leu Ala Lys His Gly Cys Arg Leu Val Leu Met Gly Asn Glu
      35      40      45
Ala Ser Leu Arg Ser Thr Val Asp Tyr Ile Arg Phe Ser Asp Asp Gly
      50      55      60
Ala Phe Pro Val Glu Leu Ile Gly Ala Asp Met Glu Ala Asp Ser Glu
      65      70      75      80
Glu Asp Phe Tyr Val Ala Val Gln Thr Ala Trp Thr Arg Leu Gly Ser
      85      90      95
Leu Asp Ala Phe Val Asn Cys Cys Thr Tyr Gln Gly Lys Met Gln Asp
      100      105      110
Ile Leu Arg Val Ser Glu Asp Glu Phe Lys Lys Ile Thr Arg Ile Asn
      115      120      125
Leu Thr Ala Thr Trp Phe Ile Leu Lys Ala Val Ala Ser Met
      130      135      140

```

<210> 19
 <211> 436
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (3)..(419)
 <223> coding for Brassica homologue H4

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<400> 19
gt cga cga ttt cgt gga gaa aac aat cta act gga aag atc caa atg 47
  Arg Arg Phe Arg Gly Glu Asn Asn Leu Thr Gly Lys Ile Gln Met
  1      5      10      15
gta tat gca gcc gag ccg gtt tgc acg ctt ttc tta aaa cat ggt cat 95
Val Tyr Ala Ala Glu Pro Val Cys Thr Leu Phe Leu Lys His Gly His
      20      25      30
gag tcg ggt tca ctc atg tcc cta ttc atg gtg cac cat agc caa gtc 143
Glu Ser Gly Ser Leu Met Ser Leu Phe Met Val His His Ser Gln Val
      35      40      45

```

```

ttt ttc gaa act tgg aca cat ttg aaa gat ctg ata caa gaa gga aaa 191
Phe Phe Glu Thr Trp Thr His Leu Lys Asp Leu Ile Gln Glu Gly Lys
      50      55      60
gat aca ttc att tct gct cat ggc atg agg atc ttt gaa tac atc ggt 239
Asp Thr Phe Ile Ser Ala His Gly Met Arg Ile Phe Glu Tyr Ile Gly
      65      70      75
ttg aat gaa caa ttc gct tgt atg ttt aac cat gca atg tca gaa tct 287
Leu Asn Glu Gln Phe Ala Cys Met Phe Asn His Ala Met Ser Glu Ser
      80      85      90      95
tct acc atg atc atg aag aag att tta gaa gtt tac aga gga ttc gaa 335
Ser Thr Met Ile Met Lys Lys Ile Leu Glu Val Tyr Arg Gly Phe Glu
      100      105      110
gat att aaa act ttg gtg gat att gga gga gga ctt ggc acc aca cta 383
Asp Ile Lys Thr Leu Val Asp Ile Gly Gly Gly Leu Gly Thr Thr Leu
      115      120      125
aat ctg gtt act tcc aag tat cct cat ata agg gta taatttcgat 429
Asn Leu Val Thr Ser Lys Tyr Pro His Ile Arg Val
      130      135
taaactc 436

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<210> 20
 <211> 139
 <212> PRT
 <213> Brassica napus

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<400> 20
Arg Arg Phe Arg Gly Glu Asn Asn Leu Thr Gly Lys Ile Gln Met Val
  1      5      10      15
Tyr Ala Ala Glu Pro Val Cys Thr Leu Phe Leu Lys His Gly His Glu
      20      25      30
Ser Gly Ser Leu Met Ser Leu Phe Met Val His His Ser Gln Val Phe
      35      40      45
Phe Glu Thr Trp Thr His Leu Lys Asp Leu Ile Gln Glu Gly Lys Asp
      50      55      60
Thr Phe Ile Ser Ala His Gly Met Arg Ile Phe Glu Tyr Ile Gly Leu
      65      70      75      80
Asn Glu Gln Phe Ala Cys Met Phe Asn His Ala Met Ser Glu Ser Ser
      85      90      95
Thr Met Ile Met Lys Lys Ile Leu Glu Val Tyr Arg Gly Phe Glu Asp
      100      105      110
Ile Lys Thr Leu Val Asp Ile Gly Gly Gly Leu Gly Thr Thr Leu Asn
      115      120      125
Leu Val Thr Ser Lys Tyr Pro His Ile Arg Val
      130      135

```

<210> 21
 <211> 418
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(417)
 <223> coding for Brassica homologue H5

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<400> 21
gct gaa ccg gtt tgc acg ctt ttt tta acc cgt ggt gac gac tcg ggt 48
Ala Glu Pro Val Cys Thr Leu Phe Leu Thr Arg Gly Asp Asp Ser Gly

```

1	5	10	15	
act cac aag tcc ctc ttc atg ttg ctc aat agc caa gta ttt ttc aag	96			
Thr His Lys Ser Leu Phe Met Leu Leu Asn Ser Gln Val Phe Phe Lys				
20 25 30				
aca tgg gat aat ctg aag ggt gtg ata caa gaa gga aaa gat gcg ttt	144			
Thr Trp Asp Asn Leu Lys Gly Val Ile Gln Glu Gly Lys Asp Ala Phe				
35 40 45				
agt tca gct cat ggc atg cca tta ttc gaa tac atc ggt ttg gat gag	192			
Ser Ser Ala His Gly Met Pro Leu Phe Glu Tyr Ile Gly Leu Asp Glu				
50 55 60				
caa ttc gct ggt atg ttt aac cat gca atg gca gaa tct tct acc atc	240			
Gln Phe Ala Gly Met Phe Asn His Ala Met Ala Glu Ser Ser Thr Ile				
65 70 75 80				
att atg aag aaa att tta gaa gtt tac aga gga ttc gaa gat gta aat	288			
Ile Met Lys Lys Ile Leu Glu Val Tyr Arg Gly Phe Glu Asp Val Asn				
85 90 95				
act ttg gtg gat att gga gga gga ctt ggc acc gta cta aac ctt gtc	336			
Thr Leu Val Asp Ile Gly Gly Gly Leu Gly Thr Val Leu Asn Leu Val				
100 105 110				
act tcc aag tat cct caa att aag ggt atc aat ttc gat tta acc atg	384			
Thr Ser Lys Tyr Pro Gln Ile Lys Gly Ile Asn Phe Asp Leu Thr Met				
115 120 125				
gtt tta gcc aat gct cct tct tat cca gga gtg g	418			
Val Leu Ala Asn Ala Pro Ser Tyr Pro Gly Val				
130 135				

<210> 22
 <211> 139
 <212> PRT
 <213> Brassica napus

<400> 22	
Ala Glu Pro Val Cys Thr Leu Phe Leu Thr Arg Gly Asp Asp Ser Gly	
1 5 10 15	
Thr His Lys Ser Leu Phe Met Leu Leu Asn Ser Gln Val Phe Phe Lys	
20 25 30	
Thr Trp Asp Asn Leu Lys Gly Val Ile Gln Glu Gly Lys Asp Ala Phe	
35 40 45	
Ser Ser Ala His Gly Met Pro Leu Phe Glu Tyr Ile Gly Leu Asp Glu	
50 55 60	
Gln Phe Ala Gly Met Phe Asn His Ala Met Ala Glu Ser Ser Thr Ile	
65 70 75 80	
Ile Met Lys Lys Ile Leu Glu Val Tyr Arg Gly Phe Glu Asp Val Asn	
85 90 95	
Thr Leu Val Asp Ile Gly Gly Gly Leu Gly Thr Val Leu Asn Leu Val	
100 105 110	
Thr Ser Lys Tyr Pro Gln Ile Lys Gly Ile Asn Phe Asp Leu Thr Met	
115 120 125	
Val Leu Ala Asn Ala Pro Ser Tyr Pro Gly Val	
130 135	

<210> 23
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: protein

motif

<220>

<221> VARIANT

<222> (4)

<223> E/Q-variation

<400> 23

Asn Gly Asp Glu Val Ser Arg Asn Ile Ala
1 5 10

<210> 24

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein
motif

<220>

<221> VARIANT

<222> (7)

<223> R/K-variation

<400> 24

Leu Ala Lys His Gly Cys Arg Leu Val
1 5

<210> 25

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein
motif

<220>

<221> unsure

<222> (5)

<223> All occurrences of Xaa indicate any amino acid

<400> 25

Met Gly Asn Glu Xaa Ser Leu Arg Ser Xaa Val Asp Xaa Ile Arg
1 5 10 15

<210> 26

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein
motif

<220>

<221> VARIANT
 <222> (14)
 <223> Q/E-variation

<400> 26
 Thr Tyr Gln Gly Lys Xaa Gln Asp Ile Leu Xaa Val Ser Gln Asp Glu
 1 5 10 15
 Phe

<210> 27
 <211> 17
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: protein
 motif

<220>
 <221> VARIANT
 <222> (3)
 <223> K/R-variation

<400> 27
 Ile Thr Lys Ile Asn Leu Thr Ala Xaa Trp Phe Xaa Leu Lys Ala Val
 1 5 10 15
 Ala

<210> 28
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: protein
 motif

<220>
 <221> unsure
 <222> (7)
 <223> All occurrences of Xaa indicate any amino acid

<400> 28
 Ala Glu Pro Val Cys Thr Xaa Phe Leu
 1 5

<210> 29
 <211> 16
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence: protein
 motif

<220>
 <221> unsure

<222> (5)

<223> All occurrences of Xaa indicate any amino acid

<400> 29

Glu	Gly	Lys	Asp	Xaa	Phe	Xaa	Ser	Ala	His	Gly	Met	Xaa	Xaa	Phe	Glu
1				5					10					15	

<210> 30

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein motif

<220>

<221> unsure

<222> (5)

<223> All occurrences of Xaa indicate any amino acid

<400> 30

Glu	Gln	Phe	Ala	Xaa	Met	Phe	Asn	Xaa	Ala	Met
1				5				10		

<210> 31

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein motif

<220>

<221> VARIANT

<222> (8)

<223> V/I-variation

<220>

<221> VARIANT

<222> (13)

<223> K/R-variation

<400> 31

Ala	Thr	Xaa	Ile	Met	Lys	Lys	Val	Leu	Glu	Val	Tyr	Lys	Gly	Phe	Glu
1				5				10						15	

Asp

<210> 32

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: protein motif

<220>
 <221> VARIANT
 <222> (5)
 <223> V/I-variation

<400> 32
 Thr Leu Val Asp Val Gly Gly Gly Xaa Gly Thr
 1 5 10

<210> 33
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 33
 cacttttccc ggcaataaca t 21

<210> 34
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 34
 atcaggaagt gatggagcat c 21

<210> 35
 <211> 19
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 35
 gaccctgtcc cacctccaa 19

<210> 36
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:
 oligonucleotide primer

<400> 36

tgagaactgc gattgtttgc a

21